

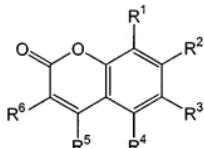
Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1-83 (canceled) .

1 **84** (previously presented): A material having a fluorogenic moiety linked to a
2 solid support, said material having the structure:



3

wherein:

4 R¹, R³, R⁴ and R⁶ are each H;

5 R² is -NHR¹⁵; and

6 R⁵ is -R¹⁴-SS,

7 wherein:

8 R¹⁴ is -CH₂C(O)NH-;

9 R¹⁵ is a member selected from the group consisting of amine protecting
10 groups, -C(O)-AA and -C(O)-P:

11 wherein:

12 P is a peptide sequence;

13 AA is an amino acid residue; and

14 SS is a solid support.

1 **85** (previously presented): The material in accordance with claim 84, wherein

2 R¹⁵ is an amine protecting group.

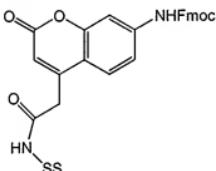
1 **86** (previously presented): The material in accordance with claim **85**, wherein
2 said amine protecting group is 9-fluorenylmethoxycarbonyl (Fmoc).

1 **87** (previously presented): The material in accordance with claim **84**, wherein
2 R¹⁵ is -C(O)-AA, wherein AA is an amino acid residue.

1 **88** (previously presented): The material in accordance with claim **84**, wherein
2 R¹⁵ is -C(O)-P, wherein P is a peptide sequence.

1 **89** (previously presented): The material in accordance with claim **84**, wherein
2 the solid support is a Rink resin.

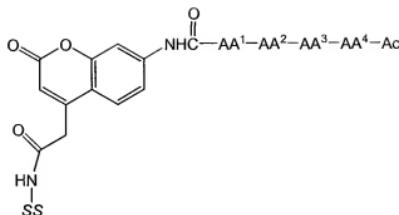
1 **90** (previously presented): A material having a fluorogenic moiety linked to a
2 solid support, said material having the structure:



3
4 wherein:

5 SS is a solid support, wherein said the support is a Rink resin.

1 **91** (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1,
2 P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides
3 having the structure:



4 wherein:

5 SS is a solid support, and

6 wherein:

7 for sub-library P1, each AA¹ is a different amino acid of the 20 amino acids, and

8 each of AA²-AA⁴ is an isokinetic mixture of 20 amino acids;

9 for sub-library P2, each of AA² is a different amino acid of the 20 amino acids,

10 and each of AA¹, AA³ and AA⁴ is an isokinetic mixture of 20 amino acids;

11 for sub-library P3, each of AA³ is a different amino acid of the 20 amino acids,

12 and each of AA¹, AA² and AA⁴ is an isokinetic mixture of 20 amino acids; and

13 for sub-library P4, each of AA⁴ is a different amino acid of the 20 amino acids,

14 and each of AA¹, AA² and AA⁴ is an isokinetic mixture of 20 amino acids.

1 **92** (withdrawn): The library in accordance with claim 91, wherein the 20 amino

2 acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

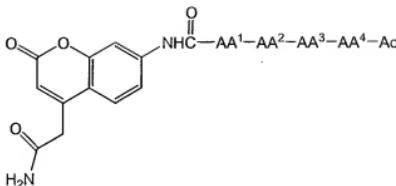
1 **93** (withdrawn): The library in accordance with claim 91, wherein the solid

2 support is a Rink resin.

1 **94** (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1,

2 P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises tetrapeptides

3 having the structure:



4 wherein:

5

6 for sub-library P1, each AA¹ is a different amino acid of the 20 amino acids, and
7 each of AA²-AA⁴ is an isokinetic mixture of 20 amino acids;

8 for sub-library P2, each of AA² is a different amino acid of the 20 amino acids,
9 and each of AA¹, AA³ and AA⁴ is an isokinetic mixture of 20 amino acids;

10 for sub-library P3, each of AA³ is a different amino acid of the 20 amino acids,
11 and each of AA¹, AA² and AA⁴ is an isokinetic mixture of 20 amino acids; and

12 for sub-library P4, each of AA⁴ is a different amino acid of the 20 amino acids,
13 and each of AA¹, AA² and AA⁴ is an isokinetic mixture of 20 amino acids.

1 **95** (withdrawn): The library in accordance with claim 94, wherein the 20 amino
2 acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

1 **96** (withdrawn): A method of determining a peptide sequence specificity profile
2 of an enzymatically active protease, said method comprising:

3 (a) contacting said protease with a library of peptides according to claim 91 or
4 claim 94 in such a manner whereby the fluorogenic moiety is released
5 from the peptide sequence, thereby forming a fluorescent moiety;

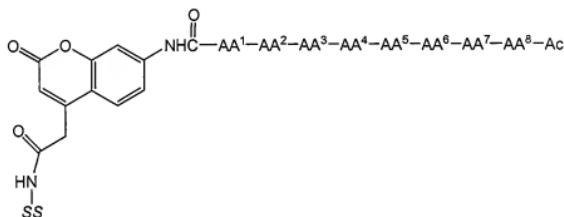
6 (b) detecting said fluorescent moiety;

7 (c) determining the sequence of said peptide sequence, thereby determining said
8 peptide sequence specificity profile of said protease.

1 **97** (withdrawn): The method according to claim **96**, further comprising (d)
2 quantifying said fluorescent moiety, thereby quantifying said protease.

1 **98** (withdrawn): The method according to claim **97**, wherein said protease is a
2 member selected from the group consisting of aspartic protease, cysteine protease,
3 metalloprotease and serine protease.

1 **99** (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1,
2 P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides
3 having the structure:



4 wherein:

5 SS is a solid support, and

6 wherein:

7 for each sub-library P1, P2, P3 and P4, AA¹, AA², AA³ and AA⁴ in each of the
8 hexapeptides are the same amino acid residues;

9 for sub-library P1, each of AA⁵ is a different amino acid of the 20 amino acids,
10 and each of AA⁶, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

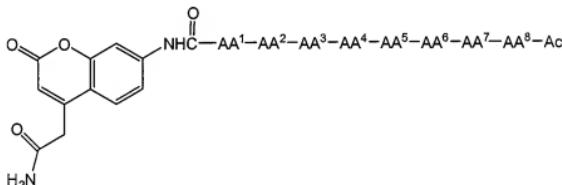
11 for sub-library P2, each of AA⁶ is a different amino acid of the 20 amino acids,
12 and each of AA⁵, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

14 for sub-library P3, each of AA⁷ is a different amino acid of the 20 amino acids,
15 and each of AA⁵, AA⁶ and AA⁸ is an isokinetic mixture of 20 amino acids; and
16 for sub-library P4, each of AA⁸ is a different amino acid of the 20 amino acids,
17 and each of AA⁵, AA⁶ and AA⁷ is an isokinetic mixture of 20 amino acids.

1 **100** (withdrawn): The library in accordance with claim 99, wherein the 20 amino
2 acids are the 20 naturally occurring amino acids excluding cysteine and including norleucine.

1 **101** (withdrawn): The library in accordance with claim 99, wherein the solid
2 support is a Rink resin.

1 **102** (withdrawn): A library of fluorogenic peptides comprising sub-libraries P1,
2 P2, P3 and P4, wherein each of the sub-libraries P1, P2, P3 and P4 comprises hexapeptides
3 having the structure:



4 wherein:
5 for each sub-library P1, P2, P3 and P4, AA¹, AA², AA³ and AA⁴ in each of the
6 hexapeptides are the same amino acid residues;

8 for sub-library P1, each of AA⁵ is a different amino acid of the 20 amino acids,
9 and each of AA⁶, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

10 for sub-library P2, each of AA⁶ is a different amino acid of the 20 amino acids,
11 and each of AA⁵, AA⁷ and AA⁸ is an isokinetic mixture of 20 amino acids;

12 for sub-library P3, each of AA⁷ is a different amino acid of the 20 amino acids,
13 and each of AA⁵, AA⁶ and AA⁸ is an isokinetic mixture of 20 amino acids; and
14 for sub-library P4, each of AA⁸ is a different amino acid of the 20 amino acids,
15 and each of AA⁵, AA⁶ and AA⁷ is an isokinetic mixture of 20 amino acids.

1 **103** (withdrawn): The library in accordance with claim 102, wherein the 20
2 amino acids are the 20 naturally occurring amino acids excluding cysteine and including
3 norleucine.

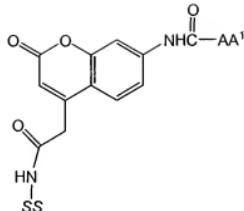
1 **104** (withdrawn): A method of determining a peptide sequence specificity profile
2 of an enzymatically active protease, said method comprising:

- 3 (a) contacting said protease with a library of peptides according to claim 99 or
4 claim 102 in such a manner whereby the fluorogenic moiety is released
5 from the peptide sequence, thereby forming a fluorescent moiety;
- 6 (b) detecting said fluorescent moiety;
- 7 (c) determining the sequence of said peptide sequence, thereby determining said
8 peptide sequence specificity profile of said protease.

1 **105** (withdrawn): The method according to claim 104, further comprising (d)
2 quantifying said fluorescent moiety, thereby quantifying said protease.

1 **106** (withdrawn): The method according to claim 105, wherein said protease is a
2 member selected from the group consisting of aspartic protease, cysteine protease,
3 metalloprotease and serine protease.

1 **107** (withdrawn): A library of twenty fluorogenic amino acid amides having the
2 structure:



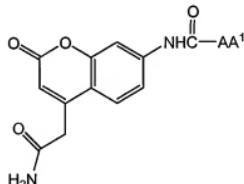
3 wherein:

4 SS is a solid support, and
5 each AA¹ for the twenty fluorogenic amino acid amides is a different amino acid
6 residue.

1 **108** (withdrawn): The library in accordance with claim 107, wherein the amino
2 acid residues are the 20 naturally occurring amino acids excluding cysteine and including
3 norleucine.

1 **109** (withdrawn): The library in accordance with claim 108, wherein the solid
2 support is a Rink resin.

1 **110** (withdrawn): A library of twenty fluorogenic amino acids having the
2 structure:



3 wherein:
4 each AA¹ for the twenty fluorogenic amino acids is a different amino acid residue

1 **111** (withdrawn): The library in accordance with claim **110**, wherein the amino
2 acid residues are the 20 naturally occurring amino acids excluding cysteine and including
3 norleucine..

1 **112** (withdrawn): A method of determining an amino acid specificity profile of
2 an enzymatically active protease, said method comprising:
3 (a) contacting said protease with a library of amino acids according to claim **108**
4 or claim **110** in such a manner whereby the fluorogenic moiety is released
5 from the amino acid, thereby forming a fluorescent moiety;
6 (b) detecting said fluorescent moiety;
7 (c) determining the identity of the amino acid, thereby determining said amino
8 acid specificity profile of said protease.

1 **113** (withdrawn): The method according to claim **112**, further comprising (d)
2 quantifying said fluorescent moiety, thereby quantifying said protease.

1 **114** (withdrawn): The method according to claim **113**, wherein said protease is a
2 member selected from the group consisting of aspartic protease, cysteine protease,
3 metalloprotease and serine protease.